

# SEQUENCE SEARCH

## SUMMARY 10/790224

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:03:48 ; Search time 173 Seconds  
(without alignments)  
1066.386 Million cell updates/sec

Title: US-10-790-224A-20

Perfect score: 2517

Sequence: 1 VAFETPEEIVKFIKDENVEF.....EISPVRLRPTPQEFLYFDC 477

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	2517	100.0	477	8	ADP87712	App EP
2	2517	100.0	477	8	ADS73714	04 EP
3	2516	100.0	477	4	AAB79682	WO PD 1/2001
4	2513	99.8	477	4	AAG93231	EP PD 6/2001
5	2036.5	80.9	478	6	ABU25851	Abu25851 Protein e
6	1790.5	71.1	478	2	AAW63035	Aaw63035 Mycobacte
7	1790.5	71.1	478	2	AAW37901	Aaw37901 Mycobacte
8	1789.5	71.1	478	7	ADF18438	Adf18438 Mycobacte
9	1784.5	70.9	478	2	AAW18160	Aaw18160 Mycobacte

10	1784.5	70.9	478	7	AAE39352	Aae39352 <i>M. tuberc</i>
11	1618	64.3	478	5	ABP65893	Abp65893 <i>Bifidobac</i>
12	1555.5	61.8	533	4	AAU54574	Aau54574 <i>Propionib</i>
13	1555.5	61.8	533	6	ABM51093	Abm51093 <i>Propionib</i>
14	1253.5	49.8	469	6	ABU49639	Abu49639 <i>Protein e</i>
15	1236.5	49.1	471	6	ABU19549	Abu19549 <i>Protein e</i>
16	1235.5	49.1	499	6	ABU23390	Abu23390 <i>Protein e</i>
17	1234.5	49.0	469	6	ABU33405	Abu33405 <i>Protein e</i>
18	1232.5	49.0	469	6	ABU28077	Abu28077 <i>Protein e</i>
19	1230.5	48.9	470	6	ABM70321	Abm70321 <i>Photorhab</i>
20	1227.5	48.8	469	6	ABU50092	Abu50092 <i>Protein e</i>
21	1226.5	48.7	471	6	ABU22059	Abu22059 <i>Protein e</i>
22	1223.5	48.6	469	6	ABU31549	Abu31549 <i>Protein e</i>
23	1221.5	48.5	476	7	ABO65700	Abo65700 <i>Klebsiell</i>
24	1216.5	48.3	469	4	AAU38196	Aau38196 <i>Salmonell</i>
25	1216.5	48.3	469	6	ABU48136	Abu48136 <i>Protein e</i>
26	1215.5	48.3	468	7	ADI53075	Adi53075 <i>E. coli g</i>
27	1215.5	48.3	469	4	AAU34825	Aau34825 <i>E. coli c</i>
28	1215.5	48.3	469	6	ABU28844	Abu28844 <i>Protein e</i>
29	1215.5	48.3	469	8	ADI38944	Adi38944 <i>Glutamine</i>
30	1214.5	48.3	469	6	ABU45561	Abu45561 <i>Protein e</i>
31	1201.5	47.7	469	6	ABU40915	Abu40915 <i>Protein e</i>
32	1201.5	47.7	493	7	ADF06469	Adf06469 <i>Bacterial</i>
33	1188	47.2	468	6	ABU40023	Abu40023 <i>Protein e</i>
34	1181	46.9	511	6	ABU37246	Abu37246 <i>Protein e</i>
35	1181	46.9	524	6	ABP80864	Abp80864 <i>N. gonorr</i>
36	1176	46.7	468	6	ABU41641	Abu41641 <i>Protein e</i>
37	1176	46.7	472	6	ABU38151	Abu38151 <i>Protein e</i>
38	1173	46.6	472	8	ADP08211	Adp08211 <i>Neisseria</i>
39	1165	46.3	469	4	AAU36495	Aau36495 <i>Pseudomon</i>
40	1165	46.3	469	6	ABU38863	Abu38863 <i>Protein e</i>
41	1163	46.2	471	6	ABU16678	Abu16678 <i>Protein e</i>
42	1163	46.2	489	6	ADA33076	Ada33076 <i>Acinetoba</i>
43	1159.5	46.1	472	4	AAU35544	Aau35544 <i>Haemophil</i>
44	1159.5	46.1	472	6	ABU30408	Abu30408 <i>Protein e</i>
45	1159.5	46.1	472	6	ABU39284	Abu39284 <i>Protein e</i>

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:13:35 ; Search time 43 Seconds  
(without alignments)  
828.084 Million cell updates/sec

Title: US-10-790-224A-20

Perfect score: 2517

Sequence: 1 VAFETPEEIVKFIKDENVEF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1221.5	48.5	476	4	US-09-489-039A-12217	Sequence 12217, A
2	1201.5	47.7	493	4	US-09-543-681A-6754	Sequence 6754, Ap
3	1163	46.2	489	4	US-09-328-352-4363	Sequence 4363, Ap
4	1153.5	45.8	481	4	US-09-252-991A-32811	Sequence 32811, A
5	1122	44.6	476	4	US-09-540-236-2406	Sequence 2406, Ap
6	722.5	28.7	448	4	US-09-583-110-4662	Sequence 4662, Ap
7	722	28.7	446	4	US-09-710-279-2250	Sequence 2250, Ap
8	722	28.7	452	3	US-09-134-001C-4173	Sequence 4173, Ap
9	499	19.8	241	4	US-09-134-000C-4967	Sequence 4967, Ap
10	457	18.2	531	4	US-09-252-991A-26690	Sequence 26690, A
11	430	17.1	275	4	US-09-107-532A-6200	Sequence 6200, Ap

12	429.5	17.1	479	4	US-09-902-540-15979	Sequence 15979, A
13	407.5	16.2	464	4	US-09-252-991A-27559	Sequence 27559, A
14	405.5	16.1	250	4	US-09-107-433-4225	Sequence 4225, Ap
15	401.5	16.0	489	4	US-09-252-991A-27833	Sequence 27833, A
16	388	15.4	464	4	US-09-252-991A-28048	Sequence 28048, A
17	348	13.8	190	4	US-09-107-532A-4613	Sequence 4613, Ap
18	341	13.5	449	4	US-09-252-991A-17901	Sequence 17901, A
19	338.5	13.4	491	4	US-09-252-991A-19014	Sequence 19014, A
20	313.5	12.5	661	4	US-09-252-991A-18960	Sequence 18960, A
21	275.5	10.9	480	4	US-09-328-352-6949	Sequence 6949, Ap
22	268.5	10.7	520	4	US-09-949-016-7107	Sequence 7107, Ap
23	249.5	9.9	1037	4	US-09-252-991A-16796	Sequence 16796, A
24	242	9.6	208	4	US-09-902-540-9748	Sequence 9748, Ap
25	222.5	8.8	257	4	US-09-489-039A-7508	Sequence 7508, Ap
26	157.5	6.3	97	4	US-09-107-433-4285	Sequence 4285, Ap
27	156	6.2	401	4	US-09-949-016-7956	Sequence 7956, Ap
28	139.5	5.5	356	4	US-09-786-534-2	Sequence 2, Appl
29	132	5.2	383	4	US-09-248-796A-17492	Sequence 17492, A
30	129	5.1	387	4	US-09-270-767-42090	Sequence 42090, A
31	104.5	4.2	796	4	US-09-107-532A-7065	Sequence 7065, Ap
32	104	4.1	139	4	US-09-107-433-4038	Sequence 4038, Ap
33	101.5	4.0	599	4	US-09-543-681A-4524	Sequence 4524, Ap
34	100	4.0	232	4	US-09-489-039A-7457	Sequence 7457, Ap
35	99.5	4.0	760	3	US-09-323-872A-31	Sequence 31, Appl
36	99.5	4.0	760	4	US-09-072-433-35	Sequence 35, Appl
37	99	3.9	3290	4	US-09-328-352-5486	Sequence 5486, Ap
38	98.5	3.9	765	4	US-09-489-039A-12098	Sequence 12098, A
39	98	3.9	452	1	US-08-434-702-6	Sequence 6, Appl
40	98	3.9	452	1	US-08-271-883-6	Sequence 6, Appl
41	96	3.8	1548	4	US-09-252-991A-22301	Sequence 22301, A
42	95	3.8	3724	2	US-08-804-227C-10	Sequence 10, Appl
43	95	3.8	3724	2	US-08-804-198-4	Sequence 4, Appl
44	94	3.7	448	4	US-09-878-766A-22	Sequence 22, Appl
45	93	3.7	854	4	US-09-949-016-11363	Sequence 11363, A

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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:19:50 ; Search time 143 Seconds  
(without alignments)  
1106.082 Million cell updates/sec

Title: US-10-790-224A-20

Perfect score: 2517

Sequence: 1 VAFETPEEIVKFIFDENVEF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%
Query	

No.	Score	Match	Length	DB	ID	Description
1	2517	100.0	477	16	US-10-720-177-4	Sequence 4, Appli
2	2517	100.0	477	17	US-10-790-224A-20	Sequence 20, Appli
3	2513	99.8	477	9	US-09-738-626-6985	Sequence 6985, Ap
4	2036.5	80.9	478	15	US-10-282-122A-53775	Sequence 53775, A
5	1642.5	65.3	469	14	US-10-156-761-13532	Sequence 13532, A
6	1253.5	49.8	469	15	US-10-282-122A-77563	Sequence 77563, A
7	1236.5	49.1	471	15	US-10-282-122A-47473	Sequence 47473, A
8	1235.5	49.1	499	15	US-10-282-122A-51314	Sequence 51314, A
9	1234.5	49.0	469	15	US-10-282-122A-61329	Sequence 61329, A
10	1232.5	49.0	469	15	US-10-282-122A-56001	Sequence 56001, A
11	1227.5	48.8	469	15	US-10-282-122A-78016	Sequence 78016, A
12	1226.5	48.7	471	15	US-10-282-122A-49983	Sequence 49983, A
13	1223.5	48.6	469	15	US-10-282-122A-59473	Sequence 59473, A
14	1216.5	48.3	469	9	US-09-815-242-13789	Sequence 13789, A
15	1216.5	48.3	469	15	US-10-282-122A-76060	Sequence 76060, A
16	1215.5	48.3	468	14	US-10-299-799-1	Sequence 1, Appli
17	1215.5	48.3	469	9	US-09-815-242-10418	Sequence 10418, A
18	1215.5	48.3	469	15	US-10-282-122A-56768	Sequence 56768, A
19	1215.5	48.3	469	15	US-10-612-779-89	Sequence 89, Appli
20	1214.5	48.3	469	15	US-10-282-122A-73485	Sequence 73485, A
21	1201.5	47.7	469	15	US-10-282-122A-68839	Sequence 68839, A
22	1188	47.2	468	15	US-10-282-122A-67947	Sequence 67947, A
23	1181	46.9	511	15	US-10-282-122A-65170	Sequence 65170, A
24	1176	46.7	468	15	US-10-282-122A-69565	Sequence 69565, A
25	1176	46.7	472	15	US-10-282-122A-66075	Sequence 66075, A
26	1165	46.3	469	9	US-09-815-242-12088	Sequence 12088, A
27	1165	46.3	469	15	US-10-282-122A-66787	Sequence 66787, A
28	1163	46.2	471	15	US-10-282-122A-44602	Sequence 44602, A
29	1159.5	46.1	472	9	US-09-815-242-11137	Sequence 11137, A
30	1159.5	46.1	472	15	US-10-282-122A-58332	Sequence 58332, A
31	1159.5	46.1	472	15	US-10-282-122A-67208	Sequence 67208, A
32	1139.5	45.3	448	15	US-10-282-122A-49184	Sequence 49184, A
33	1122	44.6	469	15	US-10-282-122A-63077	Sequence 63077, A
34	1086.5	43.2	476	15	US-10-282-122A-54398	Sequence 54398, A
35	1048	41.6	481	9	US-09-815-242-11507	Sequence 11507, A
36	1048	41.6	481	15	US-10-282-122A-58725	Sequence 58725, A
37	1048	41.6	481	15	US-10-335-977-6523	Sequence 6523, Ap
38	811	32.2	446	15	US-10-282-122A-58019	Sequence 58019, A
39	803.5	31.9	444	15	US-10-282-122A-45823	Sequence 45823, A
40	787	31.3	446	15	US-10-282-122A-57203	Sequence 57203, A
41	787	31.3	451	9	US-09-815-242-10514	Sequence 10514, A
42	782.5	31.1	444	15	US-10-282-122A-45990	Sequence 45990, A
43	765	30.4	439	15	US-10-369-493-2983	Sequence 2983, Ap
44	762.5	30.3	448	15	US-10-282-122A-72256	Sequence 72256, A
45	753	29.9	444	15	US-10-282-122A-60735	Sequence 60735, A

09/18/86  
6985

## ALIGNMENTS

RESULT 1

US-10-720-177-4

; Sequence 4, Application US/10720177  
; Publication No. US20040152175A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, Jun  
; APPLICANT: AKIYAMA, Kayo  
; TITLE OF INVENTION: Method for Producing L-Glutamine and L-Glutamine  
Producing Bacteria  
; FILE REFERENCE: OP1637-US  
; CURRENT APPLICATION NUMBER: US/10/720,177  
; CURRENT FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: JP 2002-342287  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Brevibacterium flavum

US-10-720-177-4

Query Match 100.0%; Score 2517; DB 16; Length 477;  
Best Local Similarity 100.0%; Pred. No. 1.5e-228;  
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAFETPEEIVKFIKDENVEFVDVRFTDLPGTEQHFSIPAASFDADTVEEGLAFDGSSIRG 60  
Db 1 VAFETPEEIVKFIKDENVEFVDVRFTDLPGTEQHFSIPAASFDADTVEEGLAFDGSSIRG 60

Qy 61 FTTIDESDMNLLPDLGTATLDPFRKAKTLNVKFFVHDPTREAFSRDPRNVARKAEQYLA 120  
Db 61 FTTIDESDMNLLPDLGTATLDPFRKAKTLNVKFFVHDPTREAFSRDPRNVARKAEQYLA 120

Qy 121 STGIADTCNFGAEAEFYLFDSVRYSTEMNSGFYEVDEEGWWNRKGETNLGTPNLGAKN 180  
Db 121 STGIADTCNFGAEAEFYLFDSVRYSTEMNSGFYEVDEEGWWNRKGETNLGTPNLGAKN 180

Qy 181 RVKGGYFPVAPYDQTVDVRDDMVRNLAASGFALERFHHEVGGQQEINYRFNTMLHAADD 240  
Db 181 RVKGGYFPVAPYDQTVDVRDDMVRNLAASGFALERFHHEVGGQQEINYRFNTMLHAADD 240

Qy 241 IQTFKYIIKNTARLHGKAATFMPKPLAGDNGSGMHAHQSLWKGKPLFHDESGYAGLSDI 300  
Db 241 IQTFKYIIKNTARLHGKAATFMPKPLAGDNGSGMHAHQSLWKGKPLFHDESGYAGLSDI 300

Qy 301 ARYYIGGILHHAGAVLAFTNATLNSYHRLVPGFEAPINLVYSQRNRSAAVRIPIGSNPK 360  
Db 301 ARYYIGGILHHAGAVLAFTNATLNSYHRLVPGFEAPINLVYSQRNRSAAVRIPIGSNPK 360

Qy 361 AKRIEFRAPDPSGNPYLGFAAMMMAGLDGIKNRIEPHAPVDKDLYELPPEEAASIPQAPT 420  
Db 361 AKRIEFRAPDPSGNPYLGFAAMMMAGLDGIKNRIEPHAPVDKDLYELPPEEAASIPQAPT 420

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:04:39 ; Search time 45 Seconds  
(without alignments)  
1019.898 Million cell updates/sec

Title: US-10-790-224A-20

Perfect score: 2517

Sequence: 1 VAFETPEEIVKFIKDENVEF.....EISPVRLRPTPQEFLYFDC 477

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pirl:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1789.5	71.1	478	2	H70775	probable glutamine
2	1654.5	65.7	469	1	AJSMQC	glutamate-ammonia
3	1592.5	63.3	469	2	S32024	glutamate-ammonia
4	1516	60.2	474	2	A40598	glutamate-ammonia
5	1412.5	56.1	473	2	S75141	glutamate-ammonia
6	1394	55.4	471	2	JC1403	glutamate-ammonia
7	1380.5	54.8	473	2	A47050	glutamate-ammonia
8	1363.5	54.2	474	1	AJAIQ	glutamate-ammonia
9	1363.5	54.2	474	2	AI2096	glutamate-ammonia
10	1266	50.3	469	2	G70310	glutamate-ammonia
11	1253.5	49.8	469	2	A82038	glutamate-ammonia
12	1252	49.7	468	1	AJVCQA	glutamate-ammonia
13	1227.5	48.8	469	2	AI0003	glutamate-ammonia

14	1223.5	48.6	469	1	AJEBQT	glutamate-ammonia
15	1216.5	48.3	469	2	AI0949	glutamine syntheta
16	1215.5	48.3	469	1	AJECQ	glutamate-ammonia
17	1215.5	48.3	469	2	H91227	glutamine syntheta
18	1211.5	48.1	469	2	G86074	glutamine syntheta
19	1211	48.1	469	2	AC2794	glutamine syntheta
20	1211	48.1	469	2	B97573	glutamine syntheta
21	1204.5	47.9	469	2	S23899	glutamate-ammonia
22	1197.5	47.6	468	1	AJKCQB	glutamate-ammonia
23	1184	47.0	468	2	A37176	glutamate-ammonia
24	1182.5	47.0	467	1	AJAVQ	glutamate-ammonia
25	1176	46.7	472	2	E81784	glutamate-ammonia
26	1173	46.6	472	2	F81208	glutamate-ammonia
27	1171.5	46.5	504	2	G82631	glutamine syntheta
28	1166	46.3	468	1	AJBCQF	glutamate-ammonia
29	1165	46.3	469	2	G83005	glutamine syntheta
30	1162	46.2	469	2	AE3374	glutamate-ammonia
31	1159.5	46.1	472	2	I64098	glutamate-ammonia
32	1159	46.0	469	2	D87493	glutamine syntheta
33	1148	45.6	467	2	S33181	glutamate-ammonia
34	1132	45.0	469	1	AJZRQL	glutamate-ammonia
35	1086.5	43.2	476	2	F81340	glutamate-ammonia
36	1048	41.6	481	2	B71929	glutamine syntheta
37	1048	41.6	481	2	H64583	glutamine syntheta
38	957.5	38.0	471	2	A99180	hypothetical prote
39	956.5	38.0	471	2	S11899	glutamate-ammonia
40	806.5	32.0	444	1	AJBSQU	glutamate-ammonia
41	805.5	32.0	491	2	E69368	glutamine syntheta
42	793	31.5	444	1	AJBSQS	glutamate-ammonia
43	780.5	31.0	454	2	A64468	glutamate-ammonia
44	765	30.4	439	2	B72313	glutamine syntheta
45	763	30.3	446	2	T46736	glutamate-ammonia

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 1, 2005, 19:12:54 ; Search time 182 Seconds  
(without alignments)  
1342.098 Million cell updates/sec

Title: US-10-790-224A-20

Perfect score: 2517

Sequence: 1 VAFETPEEIVKFIKDENVEF.....EISPVRLRPTPQEFELYFDC 477

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2513	99.8	477	2	Q79VE3 <i>complete seq</i>	Q79ve3 corynebacte
2	2457	97.6	477	2	Q9Z474	Q9z474 corynebacte
3	2378	94.5	477	2	Q8FNPO	Q8fnpo corynebacte
4	2036.5	80.9	478	2	Q6NG84	Q6ng84 corynebacte
5	1888.5	75.0	481	2	Q8FNM8	Q8fnm8 corynebacte
6	1838.5	73.0	478	2	Q939T2	Q939t2 mycobacteri
7	1789.5	71.1	478	1	GLN1_MYCTU	Q10377 mycobacteri
8	1778.5	70.7	478	2	Q9CCD8	Q9ccd8 mycobacteri
9	1777.5	70.6	478	2	Q73YJ4	Q73yj4 mycobacteri
10	1689	67.1	466	2	Q85177	Q85177 amycolatops
11	1654.5	65.7	469	1	GLNA_STRCO	P15106 streptomyc
12	1642.5	65.3	469	2	Q82AQ1	Q82aq1 streptomyc
13	1637.5	65.1	469	1	GLN1_STRRP	P77958 streptomyc
14	1618	64.3	478	2	Q8G5D8	Q8g5d8 bifidobacte
15	1598	63.5	474	2	Q6AFH0	Q6afh0 leifsonia x

16	1592.5	63.3	469	1	GLN1_STRVR	Q05542 streptomyce
17	1555.5	61.8	473	2	Q6A9Y9	Q6a9y9 propionibac
18	1522	60.5	474	1	GLN1_FRAAL	P46033 frankia aln
19	1421	56.5	472	2	Q7NLR9	Q7nlr9 gloeobacter
20	1398.5	55.6	473	1	GLNA_SYN3	P77961 synechocyst
21	1397	55.5	470	2	Q74C40	Q74c40 geobacter s
22	1394	55.4	470	1	GLNA_FREDI	P33035 fremyella d
23	1380.5	54.8	473	1	GLNA_SYN2	P28605 synechococc
24	1376	54.7	471	2	Q8DIJ7	Q8dij7 synechococc
25	1363.5	54.2	473	1	GLNA_ANASP	P00964 anabaena sp
26	1357.5	53.9	476	2	Q89KR8	Q89kr8 bradyrhizob
27	1345.5	53.5	473	2	O50210	O50210 synechococc
28	1337	53.1	470	2	Q6MR33	Q6mr33 bdellovibri
29	1326.5	52.7	474	2	Q9RHZ1	Q9rhz1 anabaena az
30	1321.5	52.5	473	2	Q7V1F3	Q7v1f3 prochloroco
31	1313.5	52.2	491	2	Q8XRG8	Q8xrg8 ralstonia s
32	1311.5	52.1	473	2	Q7VBQ4	Q7vbq4 prochloroco
33	1310.5	52.1	473	2	Q7U7B2	Q7u7b2 synechococc
34	1310	52.0	474	2	Q83HM2	Q83hm2 tropheryma
35	1310	52.0	482	2	Q83GK6	Q83gk6 tropheryma
36	1301.5	51.7	473	2	Q7V7X8	Q7v7x8 prochloroco
37	1293.5	51.4	473	2	O31044	O31044 synechococc
38	1274.5	50.6	469	2	Q87TE8	Q87te8 vibrio para
39	1266	50.3	469	1	GLNA_AQUAE	O66514 aquifex aeo
40	1253.5	49.8	469	1	GLNA_VIBCH	Q9knj2 vibrio chol
41	1253.5	49.8	469	2	Q7MQ11	Q7mq11 vibrio vuln
42	1253.5	49.8	469	2	Q8DDR8	Q8ddr8 vibrio vuln
43	1252	49.7	468	1	GLNA_VIBAL	P19904 vibrio algi
44	1251.5	49.7	469	2	Q6LLR5	Q6llr5 photobacter
45	1242.5	49.4	469	2	Q8E976	Q8e976 shewanella